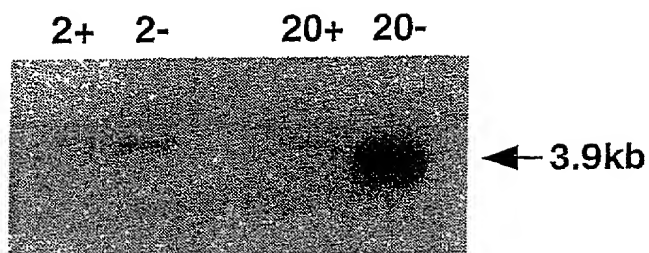


HP95	1	-----MIVADSEC-R-----AELK-----DYLFA-----PG-CWGDS-----
PA26	1	MAEGENEVRWDGLCSRDSTTRETALENIROITILRKTEYLRSVKETPHRPSDGSNTESSD
HP95	27	G-----PGEHQRES-----RAR--RGPR-----GPSAFIPVEFVLREG
PA26	61	GLNKLLAHLMLSKRCPEKQVREKSEFILKSIQELGIRIPRLGCGPSRFIPEKEFLQVG
HP95	58	AESLEQH-LGLAALMSSGRVDNAVMGLHPDYFTSFXXLHYLLHTDGPJASSWRHYIA
PA26	121	SEDAQMHALFASFAALGRDNTVMVFHQYLESEFKTQHYLLQMDGPLPLHYRHYLG
HP95	117	IMAAARHQCXYLVGSHMAEFLQTGGDPEWILLGHRAPKIKLSEINKLAHRPWLITKE
PA26	181	IMAAARHQCXYLVNLHNDLHVGGDPKWLINGLENAPQKIQNLGEINKLAHRPWLITKE
HP95	177	HTQALLKTGEHWSLAELQAVLLTHCHSLSSVFEGCGILPEGDADGSPAPQAPPPS-
PA26	241	HTQALLKAEHWSLAELQAVLLTHYHSLASFTFGCGISPEIHCDGGHTFRPPPSVSNY
HP95	236	---TQSSP-PSRD--PLN---NSGFFESARVEALMERMQLOESLLRDEG-TSQEEMES
PA26	301	CICDIINGNHSVDEMPNSAENVSVSDSFFVEALMERMQLOE--CRDEEASQEEMAS
HP95	286	RFE EKSESLVTPSADILEPSPHPDILCFVEDPTGYEDFRRGAQAPPTFRAQDYTWE
PA26	359	RFE EKRESMFVSDD-EEVTPARAVSRHEDTSYGYKDFRRGMHVP-TERVQDYQWE
HP95	346	DHGYSLLIORLYPFGGQLDEKFOAAYSLTYNTAMHSGVDTSLRRRAINWYTHCFGIRY
PA26	417	DHGYSLLIORLYPFGGQLDEKFIAYNLTYNTAMHKVDVTSLRRRAINWYTHCFGIRY
HP95	406	DDYDYGEVQQLERNIKVYIKTVACYPEKTTIRMYNLFWRHEHSEKVVHVNLLL EARMQ
PA26	477	DDYDYGEVQQLRSFKVYIKTVCTPEKVTIRMYDSFWRQEHSEKVVHVNLLL EARMQ
HP95	466	AALLYALRAITRYMT
PA26	537	AALLYALRAITRYMT

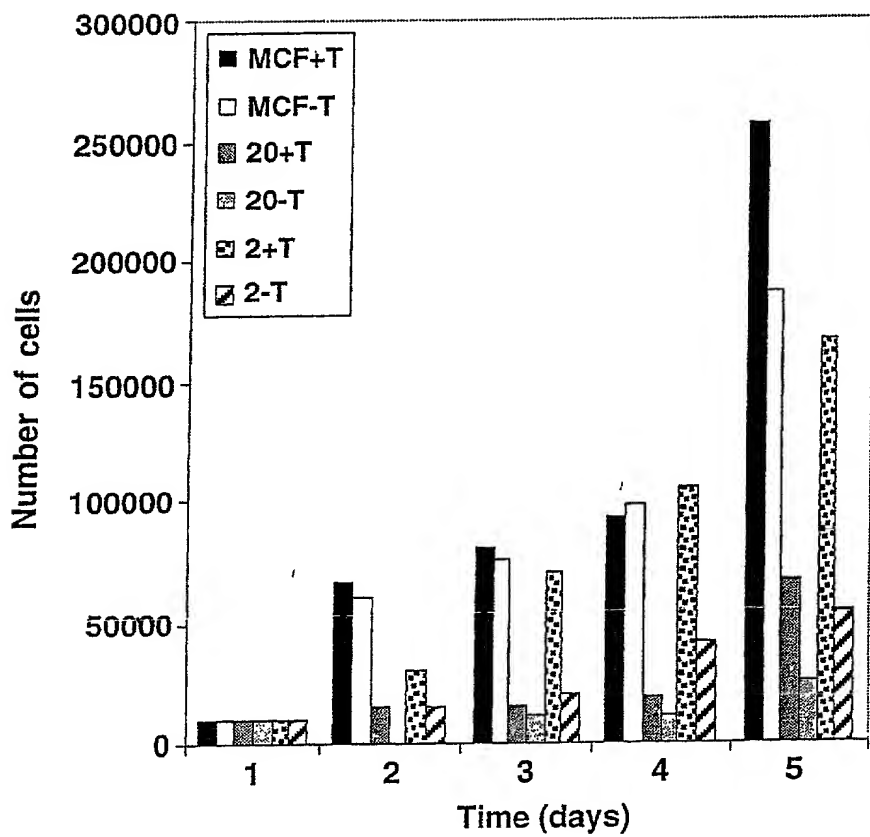
FIGURE 1

#4

**A**



**B**



**FIGURE 2**

FIG. 3

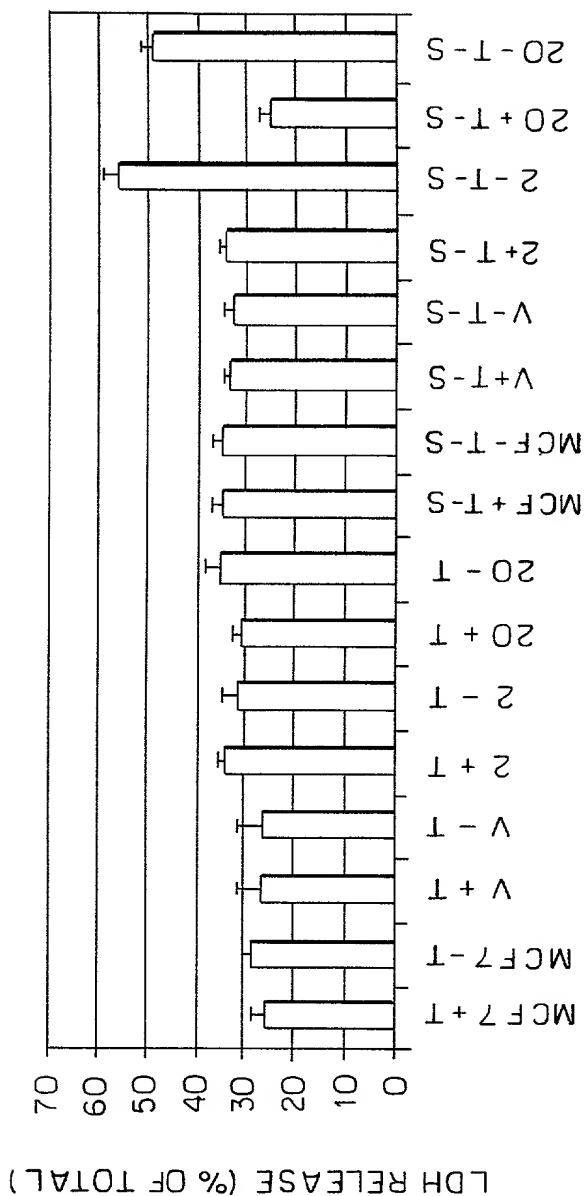
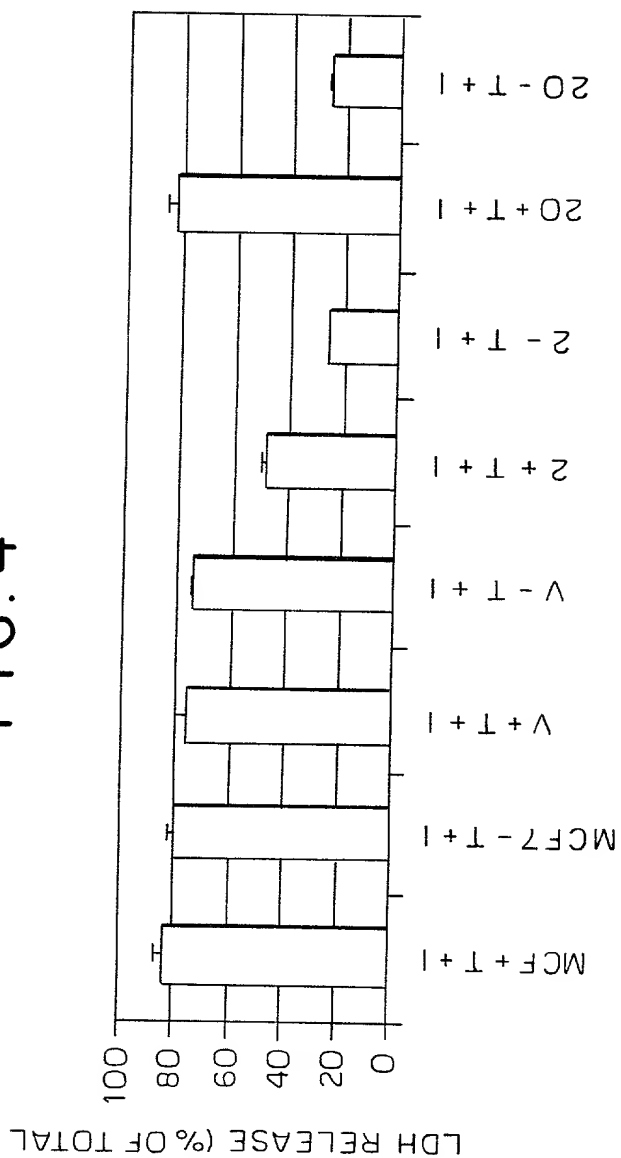


FIG. 4



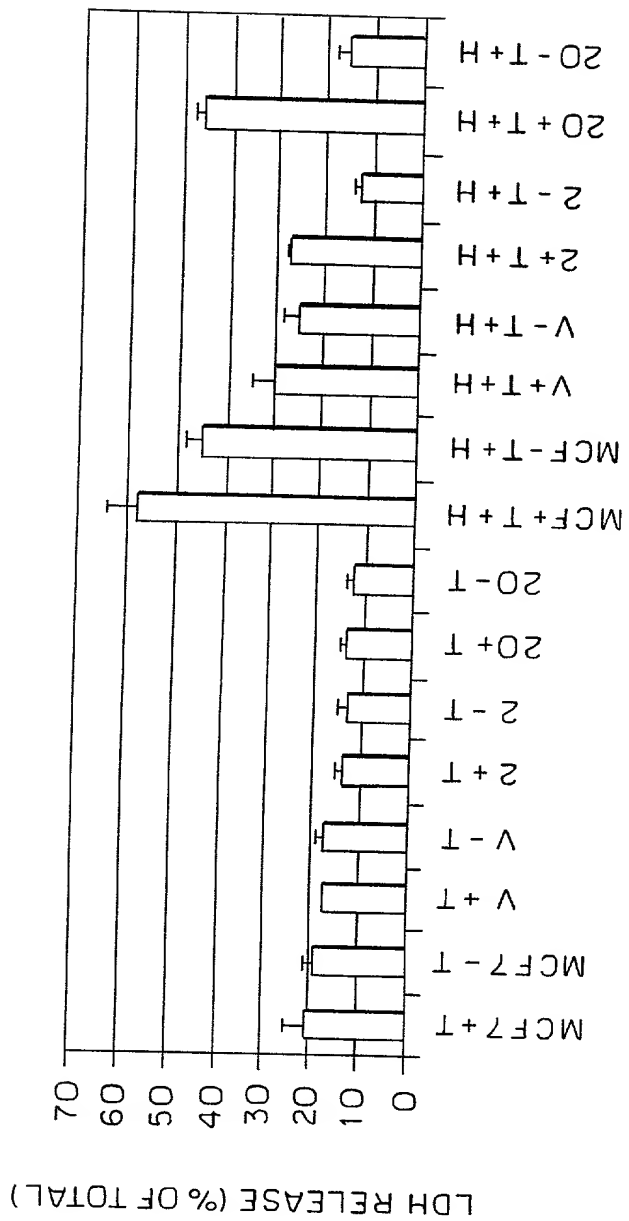


FIG. 5